

AMENDMENT

Please amend the application without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents as follows.

In the Claims

- 1-45. (Cancelled)
46. (Currently amended) An isolated polynucleotide ~~comprising 15~~ consisting of 30 contiguous nucleotides of SEQ ID No. 1 or the complement thereof ~~of SEQ ID No. 1~~.
47. (Currently amended) ~~The~~ An isolated polynucleotide consisting of claim 46 ~~wherein the polynucleotide comprises 16 contiguous nucleotides of~~ SEQ ID No. 3 ~~[[1]]~~ or the complement of SEQ ID No. 3 ~~[[1]]~~.
48. (Currently amended) ~~The~~ An isolated polynucleotide consisting of claim 46 ~~wherein the polynucleotide comprises 17 contiguous nucleotides of~~ SEQ ID No. 4 ~~[[1]]~~ or the complement of SEQ ID No. 4 ~~[[1]]~~.
49. (Currently amended) ~~The~~ An isolated polynucleotide consisting of claim 46 ~~wherein the polynucleotide comprises 18 contiguous nucleotides of~~ SEQ ID No. 5 ~~[[1]]~~ or the complement of SEQ ID No. 5 ~~[[1]]~~.
50. (Currently amended) ~~The~~ An isolated polynucleotide consisting of claim 46 ~~wherein the polynucleotide comprises 19 contiguous nucleotides of~~ SEQ ID No. 1 or the complement of SEQ ID No. 1.
51. (Cancelled)
52. (Currently amended) The polynucleotide of any one of claims 46-50, wherein the polynucleotide is DNA.
53. (Currently amended) The polynucleotide of any one of claims 46-50, wherein the polynucleotide is RNA.
54. (Currently amended) The polynucleotide of any one of claims 46-50, wherein the polynucleotide is PNA.
55. (Currently amended) ~~The~~ An isolated polynucleotide consisting of the polynucleotide of any one of claims 46-50 and further comprising a moiety that produces a signal or a binding site for a moiety that produces a signal when the polynucleotide hybridizes to *Pseudomonas* DNA.

56. (Currently amended) A kit for detecting *Pseudomonas*, comprising [[a]] one or more isolated polynucleotide(s) selected from the group consisting of SEQ ID No. 3, SEQ ID No. 4, SEQ ID No. 5, SEQ ID No. 1, 30 contiguous nucleotides of SEQ ID No. 1, and the complements thereof comprising 10 contiguous nucleotides of the *Pseudomonas* 23S/5S intergenic region.

57. (Cancelled)

58. (Currently amended) A method for detecting *Pseudomonas* in a sample, the method comprising the step of contacting the sample with determining if a first polynucleotide comprising 10 to 250 contiguous nucleotides of the *Pseudomonas* 23S/5S intergenic region, SEQ ID No. 1, or the complement of SEQ ID No. 1, hybridises to *Pseudomonas* DNA in the sample, thereby detecting *Pseudomonas* in the sample if hybridisation occurs.

59. (Currently amended) ~~The method of claim 58, further~~ A method for detecting *Pseudomonas* in a sample, the method comprising amplifying *Pseudomonas* DNA in the sample using a the first polynucleotide comprising 10 to 250 contiguous nucleotides of SEQ ID No. 1, or the complement of SEQ ID No. 1 and a second polynucleotide comprising 10 to 250 contiguous nucleotides of the *Pseudomonas* 23S/5S intergenic region, i) SEQ ID No. 1, ii) the complement of SEQ ID No. 1, iii) the 23S gene, or iv) the 5S gene, thereby detecting *Pseudomonas* in the sample if amplification occurs.

60. (Currently amended) ~~The method of claim 59~~ A method for detecting *Pseudomonas* in a sample, the method comprising amplifying *Pseudomonas* DNA using a first polynucleotide and a second polynucleotide, wherein the first polynucleotide is SEQ ID No. 3 or SEQ ID No. 5 and the second polynucleotide is SEQ ID No. 2, thereby detecting *Pseudomonas* in the sample if amplification occurs.

61. (Previously presented) The method of claim 58 wherein the first polynucleotide further comprises a moiety that produces a signal or a binding site for a moiety that produces a signal when the polynucleotide hybridizes to *Pseudomonas* DNA.

62. (Currently amended) The method of any one of claims 58-60, wherein the *Pseudomonas* is *Pseudomonas aeruginosa*.

63. (Previously presented) The method of claim 58 wherein the first polynucleotide differentially hybridizes to DNA from different strains or species of *Pseudomonas*.

64. (Currently amended) The method of claim 59 or 60 wherein the second polynucleotide differentially hybridizes to DNA from different strains or species of *Pseudomonas*.

65. (New) A kit for detecting *Pseudomonas*, comprising the polynucleotide of claim 55.

66. (New) The method of claim 56, wherein the primer or probe is SEQ ID NO:4.

67. (New) The method of claim 58 or 59, wherein the first polynucleotide comprises 15 to 30 contiguous nucleotides of SEQ ID No. 1, or the complement of SEQ ID No. 1.

68. (New) A method for producing a primer or probe for detecting the presence of one or more *Pseudomonas* strain(s) that are to be detected in a sample, wherein the method comprises:

a) comparing the sequence of the 23S/5S intergenic region of genomic DNA isolated from one or more *Pseudomonas* strain(s) that are to be detected with the sequence of the 23S/5S intergenic region of genomic DNA isolated from one or more *Pseudomonas* strain(s) that are not to be detected; and

b) selecting a nucleic acid sequence of at least 15 contiguous nucleotides that differs in at least one nucleotide position between the sequence of the 23S/5S intergenic region of the *Pseudomonas* strain(s) that are to be detected and the sequence of the 23S/5S intergenic region of the *Pseudomonas* strain(s) that are not to be detected, wherein the at least 15 contiguous nucleotides can be used as a primer or probe for detecting the presence of the one or more *Pseudomonas* strain(s) that are to be detected.

69. (New) The method of claim 68, wherein the 23S/5S intergenic region of genomic DNA has the sequence of SEQ ID NO:1.

70. (New) The method of claim 68, wherein the 23S/5S intergenic region of genomic DNA has a sequence that is at least 90% homologous to SEQ ID NO:1.

71. (New) The method of claim 68, wherein the 23S/5S intergenic region of genomic DNA comprises SEQ ID NO:5.

72. (New) The method of claim 68, wherein the primer or probe comprises SEQ ID NO:3.

73. (New) The method of claim 68, wherein the primer or probe comprises SEQ ID NO:4.

74. (New) The method of claim 68, wherein the nucleic acid sequence of b) is at least 30 contiguous nucleotides.

75. (New) The method of claim 68, wherein the nucleic acid sequence of b) is at least 250 contiguous nucleotides.

76. (New) The method of claim 68, wherein the nucleic acid sequence of b) is DNA.

77. (New) The method of claim 68, wherein the nucleic acid sequence of b) is RNA.

78. (New) The method of claim 68, wherein the nucleic acid sequence of b) is PNA.